CLAIMS

1. A method of producing a binding surface for a target molecule having a functional binding site, which method comprises:

(i) identifying within the target molecule an anchor site which is remote from the functional binding site;

(ii) generating a pharmacophore model for the anchor site;

(iii) using the pharmacophore model to identify an anchor site binding ligand; and

(iv) providing the anchor site binding ligand on a surface of a substrate such that the ability of the anchor site binding ligand to bind to the anchor site is preserved.

2. A method according to claim 1, where the anchor site is selected such that when the target molecule is bound to the binding surface, the functional binding site of the target molecule is orientated in such a way as to be available for a subsequent binding interaction with a complementary binding molecule.

3. A method according to claim 2, wherein the target molecule is a protein.

4. A method according to claim 2, wherein the target molecule is an antibody and the complementary binding molecule is an antigen.

5. A method according to claim 4, wherein the Fab fragment of the antibody corresponds to the functional binding site and the anchor site is located on the Fc fragment of the antibody.

6. A method according to claim 1, wherein anchor site is identified based on an understanding of the molecular architecture of the target molecule and on the binding characteristics of the functional binding site.

7. A method according to claim 1, wherein the pharmocophore model is a 3-D representation of molecular features defined by reference to at least four feature types.

8. A method according to claim 7, wherein the pharmacophore model is generated by reference to molecular features of the anchor site and/or by reference to molecular features of a set of one or more ligands already known to bind to the anchor site.

9. A method according to claim 7, wherein the anchor site binding ligand matches the pharmacophore model with respect to at least four feature types thereof.

10. A method according to claim 1, further comprising a docking step to ensure binding efficacy of the anchor site binding ligand to an anchor site of the target molecule.

11. A method according to claim 10, wherein the docking step is used to rank anchor site binding ligands according to their binding affinity for an anchor site of the target molecule.

12. A method according to claim 1, wherein multiple anchor site binding ligands are provided on the substrate surface to facilitate binding to respective anchor sites of the same target molecule.

13. A method according to claim 12, wherein the anchor site binding ligands are included as pendant groups on a polymer backbone that forms or is provided on the substrate surface.

14. A method according to claim 13, wherein the polymer is a copolymer of first and second monomers, wherein the first monomer is selected from styrene (optionally substituted), dimethyl, acrylamide, acrylonitrile, N,N-dimethyl (or diethyl) ethyl methacrylate, 2-methacryloyloxy-ethyl-dimethyl-3-sulfopropyl-ammounium hydroxide, and methoxy PEG and the second monomer is selected from hydroxyethyl methacrylate, maleic anhydride, N-hydroxysuccinimide methacrylate ester, methacrylic acid, diacetone acrylamide, glycidyl methacrylate, PEG methacrylate and fumarates.

15. A method according to claim 13, wherein the polymer is modified by incorporation of a spacer between the polymer backbone and the anchor site binding ligand.

16. A method according to claim 1, wherein binding of the target molecule is achieved through interaction of at least one anchor site binding ligand and an anchor site of the target molecule, in combination with non-specific binding interactions between other surface components of the substrate and the target molecule.

17. A method according to claim 1, wherein binding of the anchor site binding ligand to an anchor site of the target molecule may be manipulated by controlling prevailing environmental conditions.

18. A method according to claim 1, wherein the target molecule is IgG and the anchor site binding ligand is selected from the group consisting of 5-(4-Hydroxymethyl-3-methoxyphenoxy)valeric acid (CAS 213024-57-8), 9-Fluorenylmethoxycarbonyl-L-phenylalanine (CAS 35661-40-6), Glycocholic acid hydrate (CAS 475-31-0) and 2,4-Dinitrophenyl-alpha-aminocaproic acid (CAS 10466-72-5).

19. A method according to claim 1, wherein the target molecule is IgG and the anchor site binding ligand is selected from group consisting of Mycophenolic acid (CAS 24280-93-1), Lavendustin A (CAS 125697-92-9), Pteroic acid (CAS 119-24-4), N10-(trifluoroacetyl)pteroic acid (CAS 37793-53-6), 3-Hydroxy-4-(2-hydroxy-4-sulfo-1-naphthyl azo)naphthalene-2-carboxylic acid (CAS 3737-95-9), N-(4-Nitrobenzoyl)-6-aminocaproic acid, 5-(4-(2-Pyridylsulfamoyl)phenylazo)salicylic acid (CAS 599-79-1), 1,3,4,5-Tetrahydroxycyclohexanecarboxilic acid 3-[3,4-dihydroxycinnamate] (CAS 6001-76-9), Succinylsulfathiazole (CAS 116-43-8), Asp-Ala beta-naphthylamide, 3-carboxyumbelliferyl beta-D-galactopyranoside (CAS 64664-99-9), 4-(N-[2,4-Diamino-6-pteridinylmethyl]-N-methylamino)benzoic acid hemihydrochloride (CAS 19741-14-1), L-Glutamic acid gamma-(7-amido-4-methylcoumarin) (CAS 72669-53-5), His-Ser (CAS 21438-60-8), N-[7-Nitrobenz-2-oxa-1,3-diazol-4-yl]aminohexanoic acid (CAS 88235-25-0), Tyr-Ala (CAS 730-08-5), N-epsilon-Trifluoroacetyl-Lys-Pro (CAS 103300-89-6), N-

10-(Trifluoroacetyl)pteroic acid (CAS 37793-53-6), Ala-Trp (CAS 16305-75-2), Ala-His (CAS 3253-17-6), N-(2,4-Dinitrophenyl)-L-tryptophan (CAS 1655-51-2).

20. A binding surface that has been produced in accordance with the method as claimed in claim 1.

21. A binding surface according to claim 20, where the anchor site is selected such that when the target molecule is bound to the binding surface, the functional binding site of the target molecule is orientated in such a way as to be available for a subsequent binding interaction with a complementary binding molecule.

22. A binding surface according to claim 21, wherein the target molecule is a protein.

23. A binding surface according to claim 21, wherein the target molecule is an antibody and the complementary binding molecule is an antigen.

24. A binding surface according to claim 23, wherein the F_{ab} fragment of the antibody corresponds to the functional binding site and the anchor site is located on the Fc fragment of the antibody.

25. A binding surface according to claim 20, wherein anchor site is identified based on an understanding of the molecular architecture of the target molecule and on the binding characteristics of the functional binding site.

26. A binding surface according to claim 20, wherein the pharmocophore model is a 3-D representation of molecular features defined by reference to at least four feature types.

27. A binding surface according to claim 26, wherein the pharmacophore model is generated by reference to molecular features of the anchor site and/or by reference to molecular features of a set of one or more ligands already known to bind to the anchor site.

28. A binding surface according to claim 26, wherein the anchor site binding ligand matches the pharmacophore model with respect to at least four feature types thereof.

29. A binding surface according to claim 20, further comprising a docking step to ensure binding efficacy of the anchor site binding ligand to an anchor site of the target molecule.

30. A binding surface according to claim 29, wherein the docking step is used to rank anchor site binding ligands according to their binding affinity for an anchor site of the target molecule.

31. A binding surface according to claim 20, wherein multiple anchor site binding ligands are provided on the substrate surface to facilitate binding to respective anchor sites of the same target molecule.

32. A binding surface according to claim 31, wherein the anchor site binding ligands are included as pendant groups on a polymer backbone that is forms or is provided on the substrate surface.

33. A binding surface according to claim 32, wherein the polymer is a copolymer of first and second monomers, wherein the first monomer is selected from styrene (optionally substituted), dimethyl, acrylamide, acrylonitrile, N,N-dimethyl (or diethyl) ethyl methacrylate, 2-methacryloyloxy-ethyl-dimethyl-3-sulfopropyl-ammounium hydroxide, and methoxy PEG and the second monomer is selected from hydroxyethyl methacrylate, maleic anhydride, N-hydroxysuccinimide methacrylate ester, methacrylic acid, diacetone acrylamide, glycidyl methacrylate, PEG methacrylate and fumarates.

34. A binding surface according to claim 32, wherein the polymer is modified by incorporation of a spacer between the polymer backbone and the anchor site binding ligand.

35. A binding surface according to claim 20, wherein binding of the target molecule is achieved through interaction of at least one anchor site binding ligand and an anchor site of the target molecule, in combination with non-specific binding interactions between other surface components of the substrate and the target molecule.

36. A binding surface according to claim 20, wherein binding of the anchor site binding ligand to an anchor site of the target molecule may be manipulated by controlling prevailing environmental conditions.

37. A binding surface according to claim 20, wherein the target molecule is IgG and the anchor site binding ligand is selected from the group consisting of 5-(4-Hydroxymethyl-3-methoxyphenoxy)valeric acid (CAS 213024-57-8), 9-Fluorenylmethoxycarbonyl-L-phenylalanine (CAS 35661-40-6), Glycocholic acid hydrate (CAS 475-31-0) and 2,4-Dinitrophenyl-alpha-aminocaproic acid (CAS 10466-72-5).

38. A binding surface according to claim 20, wherein the target molecule is IgG and the anchor site binding ligand is Mycophenolic acid (CAS 24280-93-1), Lavendustin A (CAS 125697-92-9), Pteroic acid (CAS 119-24-4), N10-(trifluoroacetyl)pteroic acid (CAS 37793-53-6), 3-Hydroxy-4-(2-hydroxy-4-sulfo-1-naphthyl azo)naphthalene-2-carboxylic acid (CAS 3737-95-9), N-(4-Nitrobenzoyl)-6-aminocaproic acid, 5-(4-(2-Pyridylsulfamoyl)phenylazo)salicylic acid (CAS 599-79-1), 1,3,4,5-Tetrahydroxycyclohexanecarboxilic acid 3-[3,4-dihydroxycinnamate] (CAS 6001-76-9), Succinylsulfathiazole (CAS 116-43-8), Asp-Ala beta-naphthylamide, 3-carboxyumbelliferyl beta-D-galactopyranoside (CAS 64664-99-9), 4-(N-[2,4-Diamino-6-pteridinylmethyl]-N-methylamino)benzoic acid hemihydrochloride (CAS 19741-14-1), L-Glutamic acid gamma-(7-amido-4-methylcoumarin) (CAS 72669-53-5), His-Ser (CAS 21438-60-8), N-[7-Nitrobenz-2-oxa-1,3-diazol-4-yl]aminohexanoic acid (CAS 88235-25-0), Tyr-Ala (CAS 730-08-5), N-epsilon-Trifluoroacetyl-Lys-Pro (CAS 103300-89-6), N-10-(Trifluoroacetyl)pteroic acid (CAS 37793-53-6), Ala-Trp (CAS 16305-75-2), Ala-His (CAS 3253-17-6), N-(2,4-Dinitrophenyl)-L-tryptophan (CAS 1655-51-2).

39. A method of optimising the binding affinity of a substrate to a target molecule, which method comprises producing a binding surface on the substrate by the method as claimed in claim 1.

40. A substrate comprising a binding surface as claimed in claim 20 and a target molecule immobilised on the surface of the substrate by a binding interaction involving an anchor site of the target molecule and an anchor site binding ligand provided on the surface of the substrate.

41. Use of a substrate as claimed in claim 40 to immobilise a biological molecule that has complementary binding affinity to the target molecule.

42. Use according to claim 41 where the target molecule is a protein.

43. Use according to claim 41, wherein the target molecule is an antibody and the biological molecule is an antigen.

44. Use of a substrate as claimed in claim 40 in an immunoassay.

45. A pharmacophore model comprising at least four of the following feature types and coordinates combinations: D (19.1 ; 9.0 ; -4.2); A (14.1 ; 4.2 ; 1.5); A (17.9 ; 3.5 ; 1.5); D (19.5 ; 4.2 ; 0.1); D (23.0 ; 3.7 ; -12.4); P (23.0 ; 3.7 ; -12.4); A (17.7 ; -3.3 ; -14.1); D (20.0 ; -2.9 ; -4.8); P (20.0 ; -2.9 ; -4.8); A (18.7 ; -4.7 ; -8.7); N (18.7 ; -4.7 ; -8.7); A (18.9 ; -4.6 ; -6.6); N (18.9 ; -4.6 ; -6.6); A (17.6 ; 4.0 ; -7.9); A (16.4 ; 3.3 ; -2.7); A (15.5 ; 5.0 ; 0.0); A (17.2 ; -10.9 ; 3.3); A (18.5 ; -9.7 ; 4.6); A (19.2 ; 0.0 ; 5.6); A (15.3 ; 2.1 ; 3.5); D (15.9 ; -2.6 ; 3.8); D (16.7 ; -2.6 ; -0.9); D (14.6 ; 0.4 ; 4.6); A (18.6 ; -19.1 ; 1.3); D (13.9 ; -6.5 ; -8.5); D (18.5 ; -4.3 ; -6.1); R (18.7 ; -8.8 ; -1.7); D (13.8 ; -0.7 ; 1.2); D (22.1 ; -2.1 ; 4.6); R (20.0 ; -3.1 ; 3.1); R (18.0 ; 0.4 ; -6.7); A (14.1 ; -2.7 ; -8.5); A (20.1 ; -3.9 ; -4.5); A (18.2 ; -18.2 ; 3.3); D (18.2 ; -18.2 ; 3.3); N (19.2 ; -18.1 ; -10.8); A (18.7 ; -19.4 ; -8.7); N (18.7 ; -19.4 ; -8.7); A (18.6 ; -17.0 ; -8.7); N (18.6 ; -17.0 ; -8.7); A (19.2 ; -18.1 ; -10.8); A (15.9 ; -1.2 ; -9.6); D (18.9 ; -3.0 ; -10.4);

A (18.5 ; -4.3 ; -6.1); P (20.3 ; -13.7 ; 6.9); D (20.3 ; -13.7 ; 6.9); P (18.4 ; -15.5 ; -6.2); D (18.4 ; -15.5 ; -6.2); A (16.1 ; -4.4 ; -1.2);and A (14.3 ; -3.7 ; 1.3), where A is an hydrogen bond acceptor, D is an hydrogen bond donor, P is a positive charge, N is a negative charge and R is an aromatic feature and where the coordinates given into brackets define the relative relationship between the features with a tolerance of 2 Å for each feature.

46. Use of the pharmacophore model according to claim 45 to design a binding surface by a method as claimed in claim 1